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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
08/653,294	05/24/96	CLAYBERGER	C 286002020023

HM22/1101

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EXAMINER	
DIBRINO, M	
ART UNIT	**PAPER NUMBER**
1644	47

DATE MAILED: 11/01/01

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Offic
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Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER	
ART UNIT	PAPER NUMBER

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). **A computer readable form (CRF) of the sequence listing was submitted. However, the CRF could not be processed by the Scientific and Technical Information Center (STIC) for the reason(s) set forth on the attached CRF Diskette Problem Report.**

Applicant is given ONE MONTH, or THIRTY DAYS, whichever is longer, from the mailing date of this letter within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached CRF Diskette Problem Report with the reply.

Any inquiry concerning this communication should be directed to Examiner Ron Schwadron, Ph.D., Art Unit 1644, whose telephone number is (703) 308-4680. Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is (703) 308-0196.

RONALD B. SCHWADRON
PRIMARY EXAMINER
GROUP 1800

Ron Schwadron, Ph.D.
Art Unit 1644

Application No.: 08653294

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

RECEIVED
JUL 11 2001
TECH CENTER 1600/2900

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: 08/653,294B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2____Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3____Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4____Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5____Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6____PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7____Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8____Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9____Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10____Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11____Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12____PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/653,294B

DATE: 06/20/2001
TIME: 11:11:44

Input Set : D:\28600-20200.txt
Output Set: N:\CRF3\06202001\H653294B.raw

Does Not Comply
Corrected Diskette Needed

pgs 1-3

Please consult Sequence Rules, for valid format

```
  3 <110> APPLICANT: Stanford University
  4       Clayberger, Carol
  5       Krensky, Alan
  6       Buelow, Roland
  8 <120> TITLE OF INVENTION: IMMUNOMODULATING DIMERS
 11 <130> FILE REFERENCE: 28600-20200.23
 13 <140> CURRENT APPLICATION NUMBER: 08/653,294B
 14 <141> CURRENT FILING DATE: 1996-05-24
 16 <150> PRIOR APPLICATION NUMBER: US 08/222,851
 17 <151> PRIOR FILING DATE: 1994-04-05
 19 <150> PRIOR APPLICATION NUMBER: US 07/844,716
 20 <151> PRIOR FILING DATE: 1992-03-02
 22 <150> PRIOR APPLICATION NUMBER: US 07/755,584
 23 <151> PRIOR FILING DATE: 1991-09-03
 25 <150> PRIOR APPLICATION NUMBER: US 07/672,147
 26 <151> PRIOR FILING DATE: 1991-03-19
 28 <150> PRIOR APPLICATION NUMBER: US 07/561,246
 29 <151> PRIOR FILING DATE: 1990-07-30
 31 <150> PRIOR APPLICATION NUMBER: US 07/008,846
 32 <151> PRIOR FILING DATE: 1987-01-30
 34 <160> NUMBER OF SEQ ID NOS: 42
 36 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

ERRORED SEQUENCES

Reword the statement:
Xaa at location 2 is

Per 1.823 of Sequence Rules, the maximum number of lines in <223> response is 4; insert a <220> after the 4th line and insert <223> at beginning of 5th line

```
 38 <210> SEQ ID NO: 1
 39 <211> LENGTH: 10
 40 <212> TYPE: PRT
 41 <213> ORGANISM: Human
 43 <220> FEATURE:
 44 <221> NAME/KEY: VARIANT
 45 <222> LOCATION: (1)...(10)
 46 <223> OTHER INFORMATION: Xaa76 = E or V;
 47       Xaa77 = D,S or N;
 48       Xaa79 = R or G;
 49       Xaa80 = I or N;
W--> 50   Xaa81 is a hydrophobic or small amino acid;
W--> 51   Xaa82 = R or L;
W--> 52   Xaa83 = G or R;
W--> 53   Xaa84 = is a hydrophobic or small amino acid.
 55 <400> SEQUENCE: 1
 56 Arg Xaa76 Xaa77 Leu Xaa79 Xaa80 Xaa81 Xaa82 Xaa83 Xaa84
E--> 57  1               5                  10
 59 <210> SEQ ID NO: 2
 60 <211> LENGTH: 10
 61 <212> TYPE: PRT
```

misaligned amino acid nos - see item 3 on Error Summary Sheet

<223> invalid - do not insert numbers next to Xaa's; just show Xaa

RAW SEQUENCE LISTING DATE: 06/20/2001
PATENT APPLICATION: US/08/653,294B TIME: 11:11:44

Input Set : D:\28600-20200.txt
Output Set: N:\CRF3\06202001\H653294B.raw


```
     62 <213> ORGANISM: Human
     64 <220> FEATURE:
     65 <221> NAME/KEY: VARIANT
     66 <222> LOCATION: (1)...(10)
     67 <223> OTHER INFORMATION: Xaa76 = E or V;
     68       Xaa77 = D,S or N;
     69       Xaa79 = R or G;
     70       Xaa80 = I or N;
W--> 71       Xaa81 is a hydrophobic or small amino acid;
W--> 72       Xaa82 = R or L;
W--> 73       Xaa83 = G or R;
W--> 74       Xaa84 = is a hydrophobic or small amino acid.
     76 <400> SEQUENCE: 2
E--> 77 Xaa84 Xaa83 Xaa82 Xaa81 Xaa80 Xaa79 Leu Xaa77 Xaa76 Arg
E--> 78  1                  5                  10
     80 <210> SEQ ID NO: 3
     81 <211> LENGTH: 10
     82 <212> TYPE: PRT
     83 <213> ORGANISM: Human
     85 <220> FEATURE:
     86 <221> NAME/KEY: VARIANT
     87 <222> LOCATION: (1)...(10)
     88 <223> OTHER INFORMATION: Xaa1 = Any Amino Acid;
     89       Xaa2 = N or I; or any amino acid of at least five carbon atoms;
     90       Xaa3 = I or hydrophobic or small amino acid;
     91       Xaa4 = R or any aliphatic amino acid of at least five carbon atoms;
W--> 92       Xaa5 = G or R or any aliphatic amino acid;
W--> 93       Xaa6 = any amino acid, hydrophobic or small.
     95 <400> SEQUENCE: 3
     96 Arg Glu Xaa1 Leu Arg Xaa2 Xaa3 Xaa4 Xaa5
E--> 97  1               5                  10
    433 <210> SEQ ID NO: 38
    434 <211> LENGTH: 10
    435 <212> TYPE: PRT
    436 <213> ORGANISM: Human
    438 <220> FEATURE:
    439 <221> NAME/KEY: VARIANT
    440 <222> LOCATION: (1)...(10)
    441 <223> OTHER INFORMATION: Xaa77 = D,S or N;
    442       Xaa80 = I or N;
    443       Xaa81 = A or L;
    444       Xaa82 = R or L;
W--> 445      Xaa83 = G or R.
    447 <400> SEQUENCE: 38
E--> 448 Arg Glu Xaa77 Leu Arg Xaa80 Xaa81 Xaa82 Xaa83 Tyr
E--> 449  1               5                  10
    451 <210> SEQ ID NO: 39
    452 <211> LENGTH: 10
    453 <212> TYPE: PRT
```

same error

misaligned nos.

9 shown

same error

same error

misaligned nos.

RAW SEQUENCE LISTING DATE: 06/20/2001
PATENT APPLICATION: **US/08/653,294B** TIME: 11:11:44

Input Set : **D:\28600-20200.txt**
Output Set: **N:\CRF3\06202001\H653294B.raw**

```
     454 <213> ORGANISM: Human
     456 <220> FEATURE:
     457 <221> NAME/KEY: VARIANT
     458 <222> LOCATION: (1)...(10)
     459 <223> OTHER INFORMATION: Xaa77 = D,S or N;
     460       Xaa80 = I or N;
     461       Xaa81 = A or L;
     462       Xaa82 = R or L;
W--> 463       Xaa83 = G or R.
     465 <400> SEQUENCE: 39
E--> 466 Tyr Xaa83 Xaa82 Xaa81 Xaa80 Arg Leu Xaa77 Glu Arg ,
E--> 467  1               5                  10
```

VERIFICATION SUMMARY DATE: 06/20/2001
PATENT APPLICATION: **US/08/653,294B** TIME: 11:11:45

Input Set : **D:\28600-20200.txt**
Output Set: **N:\CRF3\06202001\H653294B.raw**

L:50 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:51 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:52 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:53 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:57 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:57 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:1
L:71 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:72 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:73 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:74 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:77 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:77 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:78 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:92 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:93 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:97 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:97 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:3
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:445 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:448 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:448 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:449 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
L:463 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:466 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:466 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:466 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:467 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39